OIPE

RAW SEQUENCE LISTING   DATE: 02/07/2002
PATENT APPLICATION: US/10/055,061   TIME: 11:09:48

Input Set : N:\Crf3\RULE60\10055061.raw
Output Set: N:\CRF3\02072002\J055061.raw

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 1 <110> APPLICANT: Bertin, John
 2 <120> TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
 3        PROTEIN FAMILY AND USES THEREOF
 4 <130> FILE REFERENCE: 07334-076001
 5 <140> CURRENT APPLICATION NUMBER: 10/055,061
 6 <141> CURRENT FILING DATE: 2002-01-22
 8 <150> PRIOR APPLICATION NUMBER: US/09/099,041A
 9 <151> PRIOR FILING DATE: 1998-06-17
12 <150> PRIOR APPLICATION NUMBER: 09/019,942
13 <151> PRIOR FILING DATE: 1998-02-06
14 <160> NUMBER OF SEQ ID NOS: 37
15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1931
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (214)...(1833)
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26       tgggcgccct cgtgacctag tgttgcgggg caaaaagggt cttgccggcc tcgctcgtgc   120
27       aggggcgtat ctgggcgcct gagcgcggcg tgggagcctt gggagccgcc gcagcagggg   180
28       gcacacccgg aaccggcctg agcgcccggg acc atg aac ggg gag gcc atc tgc    234
29                                            Met Asn Gly Glu Ala Ile Cys
30                                             1               5
31       agc gcc ctg ccc acc att ccc tac cac aaa ctc gcc gac ctg cgc tac   282
32       Ser Ala Leu Pro Thr Ile Pro Tyr His Lys Leu Ala Asp Leu Arg Tyr
33               10                  15                  20
34       ctg agc cgc ggc gcc tct ggc act gtg tcg tcc gcc cgc cac gca gac   330
35       Leu Ser Arg Gly Ala Ser Gly Thr Val Ser Ser Ala Arg His Ala Asp
36               25                  30                  35
37       tgg cgc gtc cag gtg gcc gtg aag cac ctg cac atc cac act ccg ctg   378
38       Trp Arg Val Gln Val Ala Val Lys His Leu His Ile His Thr Pro Leu
39          40                  45                  50                  55
40       ctc gac agt gaa aga aag gat gtc tta aga gaa gct gaa att tta cac   426
41       Leu Asp Ser Glu Arg Lys Asp Val Leu Arg Glu Ala Glu Ile Leu His
42                       60                  65                  70
43       aaa gct aga ttt agt tac att ctt cca att ttg gga att tgc aat gag   474
44       Lys Ala Arg Phe Ser Tyr Ile Leu Pro Ile Leu Gly Ile Cys Asn Glu
45                       75                  80                  85
46       cct gaa ttt ttg gga ata gtt act gaa tac atg cca aat gga tca tta   522
47       Pro Glu Phe Leu Gly Ile Val Thr Glu Tyr Met Pro Asn Gly Ser Leu
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48                90               95                100
49    aat gaa ctc cta cat agg aaa act gaa tat cct gat gtt gct tgg cca    570
50    Asn Glu Leu Leu His Arg Lys Thr Glu Tyr Pro Asp Val Ala Trp Pro
51        105               110               115
52    ttg aga ttt cgc atc ctg cat gaa att gcc ctt ggt gta aat tac ctg    618
53    Leu Arg Phe Arg Ile Leu His Glu Ile Ala Leu Gly Val Asn Tyr Leu
54    120               125               130               135
55    cac aat atg act cct cct tta ctt cat cat gac ttg aag act cag aat    666
56    His Asn Met Thr Pro Pro Leu Leu His His Asp Leu Lys Thr Gln Asn
57                140               145               150
58    atc tta ttg gac aat gaa ttt cat gtt aag att gca gat ttt ggt tta    714
59    Ile Leu Leu Asp Asn Glu Phe His Val Lys Ile Ala Asp Phe Gly Leu
60                155               160               165
61    tca aag tgg cgc atg atg tcc ctc tca cag tca cga agt agc aaa tct    762
62    Ser Lys Trp Arg Met Met Ser Leu Ser Gln Ser Arg Ser Ser Lys Ser
63                170               175               180
64    gca cca gaa gga ggg aca att atc tat atg cca cct gaa aac tat gaa    810
65    Ala Pro Glu Gly Gly Thr Ile Ile Tyr Met Pro Pro Glu Asn Tyr Glu
66        185               190               195
67    cct gga caa aaa tca agg gcc agt atc aag cac gat ata tat agc tat    858
68    Pro Gly Gln Lys Ser Arg Ala Ser Ile Lys His Asp Ile Tyr Ser Tyr
69    200               205               210               215
70    gca gtt atc aca tgg gaa gtg tta tcc aga aaa cag cct ttt gaa gat    906
71    Ala Val Ile Thr Trp Glu Val Leu Ser Arg Lys Gln Pro Phe Glu Asp
72                220               225               230
73    gtc acc aat cct ttg cag ata atg tat agt gtg tca caa gga cat cga    954
74    Val Thr Asn Pro Leu Gln Ile Met Tyr Ser Val Ser Gln Gly His Arg
75                235               240               245
76    cct gtt att aat gaa gaa agt ttg cca tat gat ata cct cac cga gca    1002
77    Pro Val Ile Asn Glu Glu Ser Leu Pro Tyr Asp Ile Pro His Arg Ala
78                250               255               260
79    cgt atg atc tct cta ata gaa agt gga tgg gca caa aat cca gat gaa    1050
80    Arg Met Ile Ser Leu Ile Glu Ser Gly Trp Ala Gln Asn Pro Asp Glu
81        265               270               275
82    aga cca tct ttc tta aaa tgt tta ata gaa ctt gaa cca gtt ttg aga    1098
83    Arg Pro Ser Phe Leu Lys Cys Leu Ile Glu Leu Glu Pro Val Leu Arg
84    280               285               290               295
85    aca ttt gaa gag ata act ttt ctt gaa gct gtt att cag cta aag aaa    1146
86    Thr Phe Glu Glu Ile Thr Phe Leu Glu Ala Val Ile Gln Leu Lys Lys
87                300               305               310
88    aca aag tta cag agt gtt tca agt gcc att cac cta tgt gac aag aag    1194
89    Thr Lys Leu Gln Ser Val Ser Ser Ala Ile His Leu Cys Asp Lys Lys
90                315               320               325
91    aaa atg gaa tta tct ctg aac ata cct gta aat cat ggt cca caa gag    1242
92    Lys Met Glu Leu Ser Leu Asn Ile Pro Val Asn His Gly Pro Gln Glu
93                330               335               340
94    gaa tca tgt gga tcc tct cag ctc cat gaa aat agt ggt tct cct gaa    1290
95    Glu Ser Cys Gly Ser Ser Gln Leu His Glu Asn Ser Gly Ser Pro Glu
96        345               350               355
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97          act tca agg tcc ctg cca gct cct caa gac aat gat ttt tta tct aga      1338
98          Thr Ser Arg Ser Leu Pro Ala Pro Gln Asp Asn Asp Phe Leu Ser Arg
99          360                 365                 370                 375
100         aaa gct caa gac tgt tat ttt atg aag ctg cat cac tgt cct gga aat      1386
101         Lys Ala Gln Asp Cys Tyr Phe Met Lys Leu His His Cys Pro Gly Asn
102                         380                 385                 390
103         cac agt tgg gat agc acc att tct gga tct caa agg gct gca ttc tgt      1434
104         His Ser Trp Asp Ser Thr Ile Ser Gly Ser Gln Arg Ala Ala Phe Cys
105                         395                 400                 405
106         gat cac aag acc att cca tgc tct tca gca ata ata aat cca ctc tca      1482
107         Asp His Lys Thr Ile Pro Cys Ser Ser Ala Ile Ile Asn Pro Leu Ser
108                     410                 415                 420
109         act gca gga aac tca gaa cgt ctg cag cct ggt ata gcc cag cag tgg      1530
110         Thr Ala Gly Asn Ser Glu Arg Leu Gln Pro Gly Ile Ala Gln Gln Trp
111                 425                 430                 435
112         atc cag agc aaa agg gaa gac att gtg aac caa atg aca gaa gcc tgc      1578
113         Ile Gln Ser Lys Arg Glu Asp Ile Val Asn Gln Met Thr Glu Ala Cys
114         440                 445                 450                 455
115         ctt aac cag tcg cta gat gcc ctt ctg tcc agg gac ttg atc atg aaa      1626
116         Leu Asn Gln Ser Leu Asp Ala Leu Leu Ser Arg Asp Leu Ile Met Lys
117                         460                 465                 470
118         gag gac tat gaa ctt gtt agt acc aag cct aca agg acc tca aaa gtc      1674
119         Glu Asp Tyr Glu Leu Val Ser Thr Lys Pro Thr Arg Thr Ser Lys Val
120                         475                 480                 485
121         aga caa tta cta gac act act gac atc caa gga gaa gaa ttt gcc aaa      1722
122         Arg Gln Leu Leu Asp Thr Thr Asp Ile Gln Gly Glu Glu Phe Ala Lys
123                 490                 495                 500
124         gtt ata gta caa aaa ttg aaa gat aac aaa caa atg ggt ctt cag cct      1770
125         Val Ile Val Gln Lys Leu Lys Asp Asn Lys Gln Met Gly Leu Gln Pro
126                 505                 510                 515
127         tac ccg gaa ata ctt gtg gtt tct aga tca cca tct tta aat tta ctt      1818
128         Tyr Pro Glu Ile Leu Val Val Ser Arg Ser Pro Ser Leu Asn Leu Leu
129         520                 525                 530                 535
130         caa aat aaa agc atg taagtgactg tttttcaaga agaaatgtgt ttcataaaag      1873
131         Gln Asn Lys Ser Met
132                         540
133         gatatttata aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa      1931
135 <210> SEQ ID NO: 2
136 <211> LENGTH: 540
137 <212> TYPE: PRT
138 <213> ORGANISM: Homo sapiens
139 <400> SEQUENCE: 2
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142         Lys Leu Ala Asp Leu Arg Tyr Leu Ser Arg Gly Ala Ser Gly Thr Val
143                     20                  25                  30
144         Ser Ser Ala Arg His Ala Asp Trp Arg Val Gln Val Ala Val Lys His
145                 35                  40                  45
146         Leu His Ile His Thr Pro Leu Leu Asp Ser Glu Arg Lys Asp Val Leu
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147 ·         50                   55                   60
148       Arg Glu Ala Glu Ile Leu His Lys Ala Arg Phe Ser Tyr Ile Leu Pro
149       65                   70                   75                   80
150       Ile Leu Gly Ile Cys Asn Glu Pro Glu Phe Leu Gly Ile Val Thr Glu
151                       85                   90                   95
152       Tyr Met Pro Asn Gly Ser Leu Asn Glu Leu Leu His Arg Lys Thr Glu
153                       100                  105                  110
154       Tyr Pro Asp Val Ala Trp Pro Leu Arg Phe Arg Ile Leu His Glu Ile
155                       115                  120                  125
156       Ala Leu Gly Val Asn Tyr Leu His Asn Met Thr Pro Pro Leu Leu His
157                       130                  135                  140
158       His Asp Leu Lys Thr Gln Asn Ile Leu Leu Asp Asn Glu Phe His Val
159       145                  150                  155                  160
160       Lys Ile Ala Asp Phe Gly Leu Ser Lys Trp Arg Met Met Ser Leu Ser
161                       165                  170                  175
162       Gln Ser Arg Ser Ser Lys Ser Ala Pro Glu Gly Gly Thr Ile Ile Tyr
163                       180                  185                  190
164       Met Pro Pro Glu Asn Tyr Glu Pro Gly Gln Lys Ser Arg Ala Ser Ile
165                       195                  200                  205
166       Lys His Asp Ile Tyr Ser Tyr Ala Val Ile Thr Trp Glu Val Leu Ser
167       210                  215                  220
168       Arg Lys Gln Pro Phe Glu Asp Val Thr Asn Pro Leu Gln Ile Met Tyr
169       225                  230                  235                  240
170       Ser Val Ser Gln Gly His Arg Pro Val Ile Asn Glu Glu Ser Leu Pro
171                       245                  250                  255
172       Tyr Asp Ile Pro His Arg Ala Arg Met Ile Ser Leu Ile Glu Ser Gly
173                       260                  265                  270
174       Trp Ala Gln Asn Pro Asp Glu Arg Pro Ser Phe Leu Lys Cys Leu Ile
175                       275                  280                  285
176       Glu Leu Glu Pro Val Leu Arg Thr Phe Glu Glu Ile Thr Phe Leu Glu
177                       290                  295                  300
178       Ala Val Ile Gln Leu Lys Lys Thr Lys Leu Gln Ser Val Ser Ser Ala
179       305                  310                  315                  320
180       Ile His Leu Cys Asp Lys Lys Met Glu Leu Ser Leu Asn Ile Pro
181                       325                  330                  335
182       Val Asn His Gly Pro Gln Glu Glu Ser Cys Gly Ser Ser Gln Leu His
183                       340                  345                  350
184       Glu Asn Ser Gly Ser Pro Glu Thr Ser Arg Ser Leu Pro Ala Pro Gln
185                       355                  360                  365
186       Asp Asn Asp Phe Leu Ser Arg Lys Ala Gln Asp Cys Tyr Phe Met Lys
187       370                  375                  380
188       Leu His His Cys Pro Gly Asn His Ser Trp Asp Ser Thr Ile Ser Gly
189       385                  390                  395                  400
190       Ser Gln Arg Ala Ala Phe Cys Asp His Lys Thr Ile Pro Cys Ser Ser
191                       405                  410                  415
192       Ala Ile Ile Asn Pro Leu Ser Thr Ala Gly Asn Ser Glu Arg Leu Gln
193                       420                  425                  430
194       Pro Gly Ile Ala Gln Gln Trp Ile Gln Ser Lys Arg Glu Asp Ile Val
195                       435                  440                  445
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196        Asn Gln Met Thr Glu Ala Cys Leu Asn Gln Ser Leu Asp Ala Leu Leu
197            450                 455                 460
198        Ser Arg Asp Leu Ile Met Lys Glu Asp Tyr Glu Leu Val Ser Thr Lys
199        465                 470                 475                 480
200        Pro Thr Arg Thr Ser Lys Val Arg Gln Leu Leu Asp Thr Thr Asp Ile
201                        485                 490                 495
202        Gln Gly Glu Glu Phe Ala Lys Val Ile Val Gln Lys Leu Lys Asp Asn
203                        500                 505                 510
204        Lys Gln Met Gly Leu Gln Pro Tyr Pro Glu Ile Leu Val Val Ser Arg
205                515                 520                 525
206        Ser Pro Ser Leu Asn Leu Leu Gln Asn Lys Ser Met
207            530                 535                 540
209 <210> SEQ ID NO: 3
210 <211> LENGTH: 1620
211 <212> TYPE: DNA
212 <213> ORGANISM: Homo sapiens
213 <400> SEQUENCE: 3
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216        cgcgtccagg tggccgtgaa gcacctgcac atccacactc cgctgctcga cagtgaaaga   180
217        aaggatgtct taagagaagc tgaaatttta cacaaagcta gatttagtta cattcttcca   240
218        attttgggaa tttgcaatga gcctgaattt ttgggaatag ttactgaata catgccaaat   300
219        ggatcattaa atgaactcct acataggaaa actgaatatc ctgatgttgc ttggccattg   360
220        agatttcgca tcctgcatga aattgccctt ggtgtaaatt acctgcacaa tatgactcct   420
221        cctttacttc atcatgactt gaagactcag aatatcttat tggacaatga atttcatgtt   480
222        aagattgcag attttggttt atcaaagtgg cgcatgatgt ccctctcaca gtcacgaagt   540
223        agcaaatctg caccagaagg agggacaatt atctatatgc cacctgaaaa ctatgaacct   600
224        ggacaaaaat caagggccag tatcaagcac gatatatata gctatgcagt tatcacatgg   660
225        gaagtgttat ccagaaaaca gccttttgaa gatgtcacca atcctttgca gataatgtat   720
226        agtgtgtcac aaggacatcg acctgttatt aatgaagaaa gtttgccata tgatatacct   780
227        caccgagcac gtatgatctc tctaatagaa agtggatggg cacaaaatcc agatgaaaga   840
228        ccatctttct aaaatgtttt aatagaactt gaaccagttt tgagaacatt tgaagagata   900
229        acttttcttg aagctgttat tcagctaaag aaaacaaagt tacagagtgt ttcaagtgcc   960
230        attcacctat gtgacaagaa gaaaatggaa ttatctctga acatacctgt aaatcatggt  1020
231        ccacaagagg aatcatgtgg atcctctcag ctccatgaaa atagtggttc tcctgaaact  1080
232        tcaaggtccc tgccagctcc tcaagacaat gattttttat ctagaaaagc tcaagactgt  1140
233        tattttatga agctgcatca ctgtcctgga aatcacagtt gggatagcac catttctgga  1200
234        tctcaaaggg ctgcattctg tgatcacaag accattccat gctcttcagc aataataaat  1260
235        ccactctcaa ctgcaggaaa ctcagaacgt ctgcagcctg gtatagccca gcagtggatc  1320
236        cagagcaaaa gggaagacat tgtgaaccaa atgacagaag cctgccttaa ccagtcgcta  1380
237        gatgcccttc tgtccaggga cttgatcatg aaagaggact atgaacttgt tagtaccaag  1440
238        cctacaagga cctcaaaagt cagacaatta ctagacacta ctgacatcca aggagaagaa  1500
239        tttgccaaag ttatagtaca aaaattgaaa gataacaaac aaatgggtct tcagccttac  1560
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242 <210> SEQ ID NO: 4
243 <211> LENGTH: 300
244 <212> TYPE: PRT
245 <213> ORGANISM: Homo sapiens
246 <400> SEQUENCE: 4
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